Downloaded from orbit.dtu.dk on: May 05, 2023

DTU Library

Uncovering of Classical Swine Fever Virus adaptive response to vaccination by Next Generation Sequencing

Fahnøe, Ulrik; Orton, Richard; Höper, Dirk; Beer, Martin; Rasmussen, Thomas Bruun

Publication date:
2014

Document Version
Publisher's PDF, also known as Version of record

Link back to DTU Orbit

Citation (APA):
Fahnøe, U., Orton, R., Höper, D., Beer, M., & Rasmussen, T. B. (2014). *Uncovering of Classical Swine Fever Virus adaptive response to vaccination by Next Generation Sequencing*. Abstract from 8th Annual Meeting of Epizone, Copenhagen, Denmark.

General rights
Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

EPIZONE

Abstracts

8th Annual EPIZONE Meeting

"Primed for tomorrow"

23 - 25 September 2014 in Copenhagen, Denmark
Hosted by DTU Vet

Uncovering of Classical Swine Fever Virus adaptive response to vaccination by Next Generation Sequencing

Ulrik Fahnøe[1], Richard Orton[2], Dirk Höper[3], Martin Beer[3], Thomas Bruun Rasmussen[1]

[1]*DTU Vet, National Veterinary Institute, Technical University of Denmark, Lindholm, Denmark*
[2]*Institute of Biodiversity, Animal Health, and Comparative Medicine, University of Glasgow, UK*
[3]*Institute of Diagnostic Virology, Friedrich-Loeffler-Institut, Greifswald-Insel Riems, Germany*

Next Generation Sequencing (NGS) has rapidly become the preferred technology in nucleotide sequencing, and can be applied to unravel molecular adaptation of RNA viruses such as Classical Swine Fever Virus (CSFV). However, the detection of low frequency variants within viral populations by NGS is affected by errors introduced during sample preparation and sequencing, and so far no definitive solution to this problem has been presented. Here we present NGS data from an immunisation/challenge experiment obtained by two different NGS-platforms (Ion PGM and Roche FLX). The pigs were immunised with the DIVA vaccine candidate, vR26_E2gif, and subsequently challenged with the highly virulent CSFV strain “Koslov”. NGS data of Koslov RNA derived from serum of vaccinated pigs and mock-vaccinated controls was obtained and analysed. Before low frequency analysis, we performed a rigorous error correction. Several tools were benchmarked and the RC454 developed by the Broad institute outperformed the others by removing most indels from detection and strengthened the variation detection limit. Subsequently, variation analysis revealed significant differences between the CSFV sequence data from the vaccinated and the mock-vaccinated groups. The viral sequences obtained from the mock-vaccinated pigs had a similar single-nucleotide polymorphism (SNP) distribution as the challenge virus, which was not the case for the sequence data from the vaccinated group where a complete change of the SNP distribution was observed. Additionally, new detectable non-synonymous SNPs were found in the vaccinated pigs indicating selection pressure onto the challenge virus, which was not observed in the mock-vaccinated group.